

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=9; day=10; hr=12; min=41; sec=21; ms=61;]

=====

Application No: 10587756 Version No: 20

Input Set:

Output Set:

Started: 2008-08-07 19:48:31.656
Finished: 2008-08-07 19:48:35.857
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 201 ms
Total Warnings: 3
Total Errors: 36
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

Input Set:

Output Set:

Started: 2008-08-07 19:48:31.656
Finished: 2008-08-07 19:48:35.857
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 201 ms
Total Warnings: 3
Total Errors: 36
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Miyake, Masato
Yoshikawa, Tomohiro
Mikyake, Jun

<120> EVENT SEQUENCES

<130> 690121.409USPC

<140> 10587756
<141> 2008-08-07

<150> PCT/JP2005/001151

<151> 2005-01-27

<150> JP 2004-24923

<151> 2004-01-30

<160> 46

<170> PatentIn version 3.1

<210> 1
<211> 1929
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1929)
<223> fibronectin 1

<400> 1		
atg ctt agg ggt ccg ggg ccc ggg ctg ctg ctg ctg gcc gtc cag tgc		48
Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys		
1	5	10
		15
ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag		96
Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln		
20	25	30
gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc		144
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser		
35	40	45
aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag		192
Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln		
50	55	60
tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat gga		240
Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly		
65	70	75
		80
gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act		288

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr			
85	90	95	
tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act tat			336
Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr			
100	105	110	
gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg gct			384
Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala			
115	120	125	
ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa ggg			432
Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly			
130	135	140	
ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag act			480
Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr			
145	150	155	160
ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga gaa			528
Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu			
165	170	175	
tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct ggg			576
Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly			
180	185	190	
act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc tgg			624
Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp			
195	200	205	
atg atg gta gat tgt act tgc ctg gga gaa ggc acg gga cgc atc act			672
Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr			
210	215	220	
tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc tat			720
Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr			
225	230	235	240
aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg ctc			768
Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu			
245	250	255	
cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag agg			816
Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg			
260	265	270	
cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc gat			864
His Thr Ser Val Gln Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp			
275	280	285	
gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct ccc			912
Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro			
290	295	300	
tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg atg			960
Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met			

305	310	315	320	
cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc ctg Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu				1008
325	330	335		
ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac ggt Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly				1056
340	345	350		
ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat ggc Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly				1104
355	360	365		
agg acg gac agc aca act tcg aat tat gag cag gac cag aaa tac tct Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser				1152
370	375	380		
ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser				1200
385	390	395	400	
aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr				1248
405	410	415		
act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly				1296
420	425	430		
acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met				1344
435	440	445		
gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg				1392
450	455	460		
att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg				1440
465	470	475	480	
tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr				1488
485	490	495		
tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val				1536
500	505	510		
aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys				1584
515	520	525		
aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp				1632
530	535	540		

caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca			1680
Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser			
545	550	555	560
tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc			1728
Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly			
565	570	575	
cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc			1776
Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser			
580	585	590	
tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc			1824
Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro			
595	600	605	
aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc			1872
Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser			
610	615	620	
aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt			1920
Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu			
625	630	635	640
gga tac tga			1929
Gly Tyr			

<210> 2
<211> 642
<212> PRT
<213> Homo sapiens

<400> 2

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys			
1	5	10	15

Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln			
20	25	30	

Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser			
35	40	45	

Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln			
50	55	60	

Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly			
65	70	75	80

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr
85 90 95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr
100 105 110

Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala
115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly
130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr
145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu
165 170 175

Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly
180 185 190

Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp
195 200 205

Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr
210 215 220

Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr
225 230 235 240

Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu
245 250 255

Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg
260 265 270

His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp
275 280 285

Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro
290 295 300

Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met
305 310 315 320

Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu
325 330 335

Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly
340 345 350

Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly
355 360 365

Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
370 375 380

Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
385 390 395 400

Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
405 410 415

Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
420 425 430

Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
435 440 445

Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
450 455 460

Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
465 470 475 480

Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
485 490 495

Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
500 505 510

Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
515 520 525

Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp

530 535 540

Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
545 550 555 560

Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
565 570 575

Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
580 585 590

Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
595 600 605

Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
610 615 620

Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu
625 630 635 640

Gly Tyr

<210> 3

<211> 1437

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1437)

<223> vitronectin

<400> 3

atg gca ccc ctg agg ccc ttt ttc ata cta gcc ctg gtg gca tgg gtt 48
Met Ala Pro Leu Arg Pro Phe Phe Ile Leu Ala Leu Val Ala Trp Val
1 5 10 15

tct ctg gct gac caa gag tca tgc aag ggc cgc tgc act cag ggt ttc 96
Ser Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Gln Gly Phe
20 25 30

atg gcc agc aag aag tgt cag tgt gac gag ctt tgc act tac tat cag 144
Met Ala Ser Lys Lys Cys Gln Cys Asp Glu Leu Cys Thr Tyr Tyr Gln
35 40 45

agc tgc tgt gcc gac tac atg gag cag tgc aag ccc caa gta acg cgg 192
Ser Cys Cys Ala Asp Tyr Met Glu Gln Cys Lys Pro Gln Val Thr Arg

50	55	60	
ggg gac gtg ttc act atg cca gag gat tat tgg agc tat gac tac Gly Asp Val Phe Thr Met Pro Glu Asp Asp Tyr Trp Ser Tyr Asp Tyr			240
65	70	75	80
gtg gag gag ccc aag aac aat acc aac acc ggt gtg caa ccc gag aac Val Glu Glu Pro Lys Asn Asn Thr Asn Thr Gly Val Gln Pro Glu Asn			288
85	90	95	
acc tct cca ccc ggt gac cta aat cct cgg acg gac ggc act cta aag Thr Ser Pro Pro Gly Asp Leu Asn Pro Arg Thr Asp Gly Thr Leu Lys			336
100	105	110	
ccg aca gcc ttc cta gat cct gag gaa cag cca agc acc cca gcg cct Pro Thr Ala Phe Leu Asp Pro Glu Glu Gln Pro Ser Thr Pro Ala Pro			384
115	120	125	
aaa gtg gag caa cag gag gag atc cta agg ccc gac acc act gat caa Lys Val Glu Gln Gln Glu Glu Ile Leu Arg Pro Asp Thr Thr Asp Gln			432
130	135	140	
ggg acc cct gag ttt cca gag gaa ctg tgc agt gga aag ccc ttt Gly Thr Pro Glu Phe Pro Glu Glu Leu Cys Ser Gly Lys Pro Phe			480
145	150	155	160
gac gcc ttc acg gat ctc aag aat ggg tcc ctc ttt gcc ttc cga ggg Asp Ala Phe Thr Asp Leu Lys Asn Gly Ser Leu Phe Ala Phe Arg Gly			528
165	170	175	
cag tac cgc tgt gag cta gat gag acg gca gtg agg cct ggg tac ccc Gln Tyr Arg Cys Glu Leu Asp Glu Thr Ala Val Arg Pro Gly Tyr Pro			576
180	185	190	
aaa ctt atc caa gat gtc tgg ggc att gag ggc ccc atc gat gct gcc Lys Leu Ile Gln Asp Val Trp Gly Ile Glu Gly Pro Ile Asp Ala Ala			624
195	200	205	
ttc act cgc atc aac tgt cag ggg aag acc tac ttg ttc aag ggt agt Phe Thr Arg Ile Asn Cys Gln Gly Lys Thr Tyr Leu Phe Lys Gly Ser			672
210	215	220	
cag tac tgg cgc ttt gag gat ggg gtc ctg gac cct ggt tat ccc cga Gln Tyr Trp Arg Phe Glu Asp Gly Val Leu Asp Pro Gly Tyr Pro Arg			720
225	230	235	240
aac atc tcc gaa ggc ttc agt ggc ata cca gac aat gtt gat gca gcg Asn Ile Ser Glu Gly Phe Ser Gly Ile Pro Asp Asn Val Asp Ala Ala			768
245	250	255	
ttc gcc ctt cct gcc cac cgt tac agt ggc cggt gaa agg gtc tac ttc Phe Ala Leu Pro Ala His Arg Tyr Ser Gly Arg Glu Arg Val Tyr Phe			816
260	265	270	
ttc aag ggg aag cag tac tgg gag cac gaa ttt cag cag caa ccc agc Phe Lys Gly Lys Gln Tyr Trp Glu His Glu Phe Gln Gln Pro Ser			864
275	280	285	

cag gag gag tgc gaa ggc agc tct ctg tca gcc gtg ttt gag cac ctt 912
Gln Glu Glu Cys Glu Gly Ser Ser Leu Ser Ala Val Phe Glu His Phe
290 295 300

gcc ttg ctt cag cgg gac agc tgg gag aac att ttc gaa ctc ctc ttc 960
Ala Leu Leu Gln Arg Asp Ser Trp Glu Asn Ile Phe Glu Leu Leu Phe
305 310 315 320

tgg ggc aga tcc tct gat gga gcc aga gaa ccc caa ttc atc agc cgg